



1600

RAW SEQUENCE LISTING

DATE: 04/27/2004 ✓

PATENT APPLICATION: US/09/506,079H

TIME: 09:52:36

Input Set : A:\49321-16.ST25.txt

Output Set: N:\CRF4\04272004\I506079H.raw

pg. 9

ENTERED

3 <110> APPLICANT: Clinton, Gail M.
 4 Evans, Adam
 5 Henner, William D.
 7 <120> TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
 9 <130> FILE REFERENCE: 49321-16
 11 <140> CURRENT APPLICATION NUMBER: US 09/506,079H
 12 <141> CURRENT FILING DATE: 2000-02-16
 14 <160> NUMBER OF SEQ ID NOS: 15
 16 <170> SOFTWARE: PatentIn version 3.2
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 79
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: MISC_FEATURE
 26 <222> LOCATION: (2)..(2)
 27 <223> OTHER INFORMATION: Applicants herein disclose Thr and Ser sequence variants at
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 28 position
 30 <220> FEATURE:
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 32 <222> LOCATION: (5)..(5)
 33 <223> OTHER INFORMATION: Applicants herein disclose Leu and Pro sequence variants at
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 34 position
 36 <220> FEATURE:
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 38 <222> LOCATION: (6)..(6)
 39 <223> OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at
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 40 position
 42 <220> FEATURE:
 43 <221> NAME/KEY: MISC_FEATURE
 44 <222> LOCATION: (16)..(16)
 45 <223> OTHER INFORMATION: Applicants herein disclose Leu and Gln sequence variants at
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 46 position
 48 <220> FEATURE:
 49 <221> NAME/KEY: MISC_FEATURE
 50 <222> LOCATION: (18)..(18)
 51 <223> OTHER INFORMATION: Applicants herein disclose Met and Leu sequence variants at
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 54 <220> FEATURE:

55 <221> NAME/KEY: MISC_FEATURE

56 <222> LOCATION: (21)..(21)

57 <223> OTHER INFORMATION: Applicants herein disclose Gly, Asp, Ala and Val sequence
58 variants at this position

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60 <220> FEATURE:
61 <221> NAME/KEY: MISC_FEATURE
62 <222> LOCATION: (36)..(36)
63 <223> OTHER INFORMATION: Applicants herein disclose Leu and Ile sequence variants at
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64      position
66 <220> FEATURE:
67 <221> NAME/KEY: MISC_FEATURE
68 <222> LOCATION: (54)..(54)
69 <223> OTHER INFORMATION: Applicants herein disclose Pro and Arg sequence variants at
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74 <222> LOCATION: (64)..(64)
75 <223> OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at
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76      position
78 <220> FEATURE:
79 <221> NAME/KEY: MISC_FEATURE
80 <222> LOCATION: (73)..(73)
81 <223> OTHER INFORMATION: Applicants herein disclose Asp and Asn sequence variants at
this
82      position
84 <400> SEQUENCE: 1
W--> 86 Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro Xaa
      87 1          5          10          15
      90 Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro
      91          20          25          30
      94 Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu
      95          35          40          45
      98 Ser Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val Gly Arg Gly Xaa
      99          50          55          60
     102 Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser Arg Tyr Glu Gly
     103 65          70          75
     106 <210> SEQ ID NO: 2
     107 <211> LENGTH: 419
     108 <212> TYPE: PRT
     109 <213> ORGANISM: Homo sapiens
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     114 <222> LOCATION: (342)..(342)
     115 <223> OTHER INFORMATION: Applicants herein disclose Thr and Ser sequence variants at
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     120 <222> LOCATION: (345)..(345)
     121 <223> OTHER INFORMATION: Applicants herein disclose Leu and Pro sequence variants at
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     125 <221> NAME/KEY: MISC_FEATURE

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126 <222> LOCATION: (346)..(346)

127 <223> OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at this

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128      position
130 <220> FEATURE:
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132 <222> LOCATION: (356)..(356)
133 <223> OTHER INFORMATION: Applicants herein disclose Leu and Gln sequence variants at
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136 <220> FEATURE:
137 <221> NAME/KEY: MISC_FEATURE
138 <222> LOCATION: (358)..(358)
139 <223> OTHER INFORMATION: Applicants herein disclose Met and Leu sequence variants at
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142 <220> FEATURE:
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144 <222> LOCATION: (361)..(361)
145 <223> OTHER INFORMATION: Applicants herein disclose Gly, Asp, Ala and Val sequence
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149 <221> NAME/KEY: MISC_FEATURE
150 <222> LOCATION: (376)..(376)
151 <223> OTHER INFORMATION: Applicants herein disclose Leu and Ile sequence variants at
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155 <221> NAME/KEY: MISC_FEATURE
156 <222> LOCATION: (394)..(394)
157 <223> OTHER INFORMATION: Applicants herein disclose Pro and Arg sequence variants at
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162 <222> LOCATION: (404)..(404)
163 <223> OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at
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164      position
166 <220> FEATURE:
167 <221> NAME/KEY: MISC_FEATURE
168 <222> LOCATION: (413)..(413)
169 <223> OTHER INFORMATION: Applicants herein disclose Asp and Asn sequence variants at
this
170      position
172 <400> SEQUENCE: 2
174 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
175 1          5          10          15
178 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
179          20          25          30
182 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
183          35          40          45
186 Leu Tyr Gln Gly Cys Gln Val Gln Gly Asn Leu Glu Leu Thr Tyr
187          50          55          60
190 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
191 65          70          75          80

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194	Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu
195					85					90					95	

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198 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
199          100          105          110
202 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
203          115          120          125
206 Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
207          130          135          140
210 Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
211 145          150          155          160
214 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
215          165          170          175
218 Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
219          180          185          190
222 His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
223          195          200          205
226 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
227          210          215          220
230 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
231 225          230          235          240
234 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
235          245          250          255
238 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
239          260          265          270
242 Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
243          275          280          285
246 Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
247          290          295          300
250 Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
251 305          310          315          320
254 Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
255          325          330          335
W--> 258 Pro Cys Ala Arg Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val
259          340          345          350
262 Pro Val Pro Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser
263          355          360          365
266 Phe Leu Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro
267          370          375          380
270 Leu Ala Pro Leu Asp Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val
271 385          390          395          400
274 Gly Arg Gly Xaa Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser Arg
275          405          410          415
278 Tyr Glu Gly
282 <210> SEQ ID NO: 3
283 <211> LENGTH: 19
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: HER-2-specific oligonucleotide primer
290 <400> SEQUENCE: 3
291 tgagcaccat ggagctggc

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294 <210> SEQ ID NO: 4
295 <211> LENGTH: 22
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: HER-2-specific oligonucleotide primer
302 <400> SEQUENCE: 4
303 tccggcagaa atgccaggct cc 22
306 <210> SEQ ID NO: 5
307 <211> LENGTH: 22
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: HER-2 cDNA-specific oligonucleotide primer
314 <400> SEQUENCE: 5
315 aacacagcgg tgtgagaagt gc 22
318 <210> SEQ ID NO: 6
319 <211> LENGTH: 21
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
324 <223> OTHER INFORMATION: HER-2 ECDIIIa-region-specific oligonucleotide primer
326 <400> SEQUENCE: 6
327 ataccgggac aggtcaacag c 21
330 <210> SEQ ID NO: 7
331 <211> LENGTH: 20
332 <212> TYPE: DNA
333 <213> ORGANISM: Artificial Sequence
335 <220> FEATURE:
336 <223> OTHER INFORMATION: HER-2 ECDIIIa-region-specific oligonucleotide primer
338 <400> SEQUENCE: 7
339 tctgggtacc cactcactgc 20
342 <210> SEQ ID NO: 8
343 <211> LENGTH: 22
344 <212> TYPE: DNA
345 <213> ORGANISM: Artificial Sequence
347 <220> FEATURE:
348 <223> OTHER INFORMATION: HER-2 exon-specific oligonucleotide primer
350 <400> SEQUENCE: 8
351 ttcacactgg cacgtccaga cc 22
354 <210> SEQ ID NO: 9
355 <211> LENGTH: 27
356 <212> TYPE: DNA
357 <213> ORGANISM: Artificial Sequence
359 <220> FEATURE:
360 <223> OTHER INFORMATION: HER-2 cDNA-specific oligonucleotide primer
362 <400> SEQUENCE: 9
363 gcacggatcc atagcagact gaggagg 27
366 <210> SEQ ID NO: 10

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. ~~2,5,6,16,18,21,36,54,64,73~~

Seq#:2; Xaa Pos. ~~342,345,346,356,358,361,376,394,404,413~~

Seq#:10; N Pos. 62

Seq#:10; Xaa Pos. 2,5,6,16,18,21,36,54,64,73

VERIFICATION SUMMARY

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L:86 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

M:341 Repeated in SeqNo=1

L:258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:336

M:341 Repeated in SeqNo=2

L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:48

M:341 Repeated in SeqNo=10